Amendments to the Claims:

The following listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Previously Presented) A method for assaying the presence or the absence of at least one mutation on a strand of nucleic acids paired in a duplex form, comprising:

contacting in a liquid medium said duplex, suspected to include at least one mismatch with at least one compound able to undergo a specific base pairing interaction with said mismatch, said compound(s) being used at a combined concentration of at least 10g/l in said medium; and

assaying for said mismatch by an analytical method.

2. (Original) The method according to claim 1, wherein the strands of nucleic acids paired in duplex form are two DNA strands which are in all or in part complementary.

3. (Previously Presented) A method for performing Electrophoretic Heteroduplex Analysis "EHDA" on a nucleic acid sample suspected to include at least one heteroduplex, comprising:

contacting in a liquid medium said nucleic acid sample suspected to include at least one heteroduplex, with at least one compound able to undergo a specific base pairing interaction with at least one mismatch of said heteroduplex, said compound(s) being used at a combined concentration of at least 10g/l of said medium,

assaying for the presence of said heteroduplex based on its electrophoretic mobility.

4. (Previously Presented) The method according to claim 3 comprising a preliminary step of denaturating the nucleic acid sample and renaturating it under conditions that achieve both heteroduplexes and homoduplexes.

5. (Previously Presented) A method for assaying the presence or the absence of at least one mutation on a single strand of nucleic acid in a liquid medium, comprising:

(a) contacting said nucleic acid suspected to include at least one mutation with a nucleic acid probe grafted on a solid support,

(b) allowing the hybridization of at least a part of said strand of nucleic acid with the grafted nucleic acid probe,

(c) washing non-hybridized strands, and

(d) assaying for said mutation by an analytical method,

wherein the steps a) and/or c) are performed in the presence of at least one compound able to undergo a specific base pairing interaction with said mutation, said compound being at a concentration of at least lg/l.

6. (Previously Presented) The method according to claim 1 wherein the strand(s) of nucleic acids is a single stranded DNA, RNA, LNA, PNA, or any artificial or natural analog of nucleic acids.

7. (Previously Presented) The method according to claim 1, wherein the compound able to undergo a specific base pairing interaction includes at least two groups suitable for hydrogen bonding, in an orientation, polarity and spacing compatible with a creation of attractive interaction with at least one of bases A, T, G, C, and U.

8. (Previously Presented) The method according to claim 1, wherein said compound is unable to interfere with polymerization reactions of nucleotides and/or to be incorporated into a newly polymerized DNA strand.

9. (Previously Presented) The method according to claim 1, wherein said compound is selected from the group consisting of oligonucleotides less than 5 nucleotides in length, nucleosides, bases, and mixtures thereof.

10. (Previously Presented) The method according to claim 9, wherein the oligonucleotides are less than 3 nucleotides in length.

11. (Previously Presented) The method according to claim 9, wherein the compound is selected from the group consisting of adenosine, guanosine, uridine, cytidine, thymidine, and mixtures thereof.

12. (Previously Presented) The method according to claim 9, wherein the oligonucleotides less than 5 nucleotides in length, the nucleosides, the bases, and the mixture thereof are unable to undergo base pairing interactions with each other.

13. (Previously Presented) The method according to claim 12, wherein the compound includes cytidine and thymidine, or cytidine and adenosine, or guanosine and thymidine, or guanosine and adenosine.

14. (Previously Presented) The method according to claim 1, wherein the compound(s) is used at a concentration of at least 25 g/l.

15. (Previously Presented) The method according to claim 1, wherein said compound(s) has at least one substituent.

16. (Previously Presented) The method according to claim 15, wherein said substituent induces in said compound at least one change selected from the group consisting of:

an increase in solubility,

a change in charge, and

a change in friction with a solvent.

17. (Previously Presented) The method according to claim 1, wherein the mutation is a point mutation.

18. (Previously Presented) The method according to claim 1, wherein said mutation is assayed by a hybridization assay.

19. (Previously Presented) The method according to claim 1, wherein said mutation is assayed by an electrophoretic analysis using a liquid separating medium.

20. (Previously Presented) The method according to claim 19, wherein said liquid separating medium contains at least a polymer at a concentration of at least 1% by weight of the total weight of said medium.

21. (Previously Presented) The method according to claim 19, wherein said liquid separating medium contains at least one polymer selected from the group consisting of N,N-disubstituted polyacrylamides and N- substituted polyacrylamides, wherein said N substituents are selected from the group consisting of C_1 to C_{12} alkyls, halo-substituted C_1 to C_{12} alkyls, methoxy-substituted C_1 to C_{12} alkyls, and hydroxyl-substituted C_1 to C_{12} alkyls.

22. (Previously Presented) The method according to claim 20, wherein the liquid separation medium contains at least one polymer composed of several polymer segments, said polymer being of an irregular block copolymer type or irregular comb polymer type and having on average at least three junction points established between polymer segments of different chemical or topological nature.

23. (Previously Presented) The method according to claim 22, wherein the polymer comprises at least one type of polymer segment showing, within the separating medium, specific affinity for a channel wall, and at least one type of polymer segment showing in said medium less or no affinity for said wall.

24. (Previously Presented) The method according to claim 20, wherein said polymer contains acrylamide or substituted acrylamides.

25. (Previously Presented) A method used in determining whether a patient is predisposed to a cancer or a genetic disease known to be associated or putatively associated with a specific point mutation, or used in diagnosing a patient suspected of suffering from

said cancer or disease, or used in determining a prognosis of a patient diagnosed as having said cancer or disease, the method comprising:

obtaining from the patient a nucleic acid suspected to include at least one mismatch corresponding to the specific point mutation;

placing the nucleic acid, paired in duplex form, in a liquid medium and contacting the nucleic acid with at least one compound able to undergo a specific base pairing interaction with said mismatch, said at least one compound being used at a combined concentration of at least 10g/l in said medium; and

assaying for said mismatch by an analytical method to detect whether said mismatch is present, wherein the presence of said mismatch indicates that the nucleic acid has the specific point mutation known to be associated or putatively associated with the cancer or the genetic disease.

26. (Previously Presented) The method according to claim 25, wherein said point mutation is in a human breast cancer predisposition gene (BRCA).

27. (Currently Amended) A composition comprising a compound able to undergo specific base pairing interaction at a concentration of at least 1 g/l being present in a liquid separating medium that comprises at least one ~~polymer~~ irregular block copolymer at a concentration of at least 1% by weight.

28. (Previously Presented) The composition according to claim 27, wherein the compound able to undergo a specific base pairing interaction includes at least two groups suitable for hydrogen bonding, in an orientation, polarity and spacing compatible with a creation of attractive interaction with at least one of bases A, T, G, C, and U.

29. (Canceled)

30. (Currently Amended) The composition according to claim 27, wherein said liquid ~~separation~~ separating medium comprises one member selected from the group consisting of:

sieving polymers,

hydrophilic polymers, and

surface-active polymers.

31. (Currently Amended) A composition comprising a DNA fragment having a nucleic acid sequence ~~related~~ that is hybridizable to a portion of a gene on which a point mutation(s) has been associated or putatively associated with a disease or an increased predisposition to a disease, and a compound able to undergo specific base pairing interaction, said compound being present at a concentration of at least 10g/l, wherein said compound able to undergo a specific base pairing interaction includes at least two groups suitable for hydrogen bonding, in an orientation, polarity and spacing compatible with a creation of attractive interaction with at least one of bases A, T, G, C, and U.

32. (Currently Amended) A composition comprising a compound able to undergo specific base pairing interaction, said compound being present at a concentration of at least 10 g/l, and a pair of DNA probes that are molecular beacons, wherein said compound able to undergo a specific base pairing interaction includes at least two groups suitable for hydrogen bonding, in an orientation, polarity and spacing compatible with a creation of attractive interaction with at least one of bases A, T, G, C, and U.

33. (Previously Presented) A kit useful for the screening of a nucleic acid and/or nucleic acid analogs having a sequence related to a gene on which point mutation(s) has been associated or putatively associated with a disease or an increased predisposition to a disease, said kit comprising at least one composition according to claim 27.

34. (Currently Amended) A method for assaying a nucleic acid for mutation, comprising:

performing a polymerase chain reaction on said nucleic acid in the presence of at least two primers and a pool of compounds able to undergo specific base pairing interaction with nucleotides and/or nucleotide analogues, said compounds being at a combined concentration of at least 10 g/l and being unable to ~~interfere with the polymerase chain reaction~~ be incorporated into a newly polymerized nucleic acid; and

analyzing and/or quantifying the so-obtained DNA fragments.

35. (Previously Presented) The method according to claim 34, wherein the compound able to undergo a specific base pairing interaction includes at least two groups suitable for hydrogen bonding, in an orientation, polarity and spacing compatible with a creation of attractive interaction with at least one of bases A, T, G, C, and U.

36. (Previously Presented) The method according to claim 25, wherein the method is used in determining whether a patient is predisposed to a cancer or a genetic disease known to be associated or putatively associated with a specific point mutation.

37. (Previously Presented) A method for assaying for the presence of a mismatch on a nucleic acid in duplex form, the method comprising:

contacting the nucleic acid with a composition comprising a compound able to undergo specific base pairing interaction at a concentration of at least 1 g/l present in a liquid separating medium; and

assaying for a mismatch in the nucleic acid to detect whether the mismatch is present.

38. (Previously Presented) A method for assaying for the presence of a mismatch on a nucleic acid in duplex form, the method comprising:

contacting a nucleic acid with a compound able to undergo specific base pairing interaction at a concentration of at least 10g/l; and

assaying for a mismatch in the nucleic acid to detect whether the mismatch is present;

wherein:

the nucleic acid comprises a nucleic sequence corresponding to a gene on which a point mutation is known to be associated with a disease or a predisposition to a disease; and

the compound able to undergo a specific base pairing interaction comprises at least two groups suitable for hydrogen bonding, in an orientation, polarity, and spacing compatible with a creation of attractive interaction with at least one of bases A, T, G, C, and U.

39. (Previously Presented) A method for assaying for the presence of a mismatch on a nucleic acid in duplex form, the method comprising:

contacting the nucleic acid with a composition comprising a compound able to undergo specific base pairing interaction at a concentration of at least 10 g/l and a pair of DNA probes; and

assaying for a mismatch in the nucleic acid to detect whether the mismatch is present;

wherein:

the compound able to undergo a specific base pairing interaction comprises at least two groups suitable for hydrogen bonding, in an orientation, polarity, and spacing compatible with a creation of attractive interaction with at least one of bases A, T, G, C, and U.

40. (New) The method according to claim 1, wherein said combined concentration is from 10 g/l to 75 g/l.

41. (New) The method according to claim 3, wherein said combined concentration is from 10 g/l to 75 g/l.

42. (New) The method according to claim 5, wherein said concentration is from l g/l to 75 g/l.

43. (New) The method according to claim 25, wherein said combined concentration is from 10 g/l to 75 g/l.

44. (New) The composition according to claim 27, wherein said concentration is from l g/l to 75 g/l.

45. (New) The composition according to claim 31, wherein said concentration is from l0 g/l to 75 g/l.

46. (New) The composition according to claim 32, wherein said concentration is from l0 g/l to 75 g/l.

47. (New) The method according to claim 34, wherein said combined concentration is from l0 g/l to 75 g/l.

48. (New) The method according to claim 37, wherein said concentration is from l g/l to 75 g/l.

49. (New) The method according to claim 38, wherein said concentration is from l0 g/l to 75 g/l.

50. (New) The method according to claim 39, wherein said concentration is from l0 g/l to 75 g/l.